Davis, Minh-Tam

From:

Davis, Minh-Tam

Sent:

Monday, January 09, 2006 4:08 PM

To:

Chan, Christina

Subject:

Rush search request for 10/048046

1) Please search in commercial database, issued patent files and PGPUB:

A nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.

- 2) Interference search only for:
 - a) SEQ ID NO:1
- b) oligonucleotide search for SEQ ID NO:1, with size limitation for the sequences in the database to equal or less than 50 nucleotides.
 - c) A nucleic acid encoding SEQ ID NO:2.
- d) oligonucleotide search for a nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.

Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

```
Regult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MODEL-frame+_p2n.model -DEV=xlh
-Q=/ggn2_1/USPTO_spool/US10048046/runat_10012006_122339_24142/app_query.fasta_1.839
-Q=/ggn2_1/USPTO_spool/US10048046/runat_10012006_122339_24142/app_query.fasta_1.839
-DB=168ued_patence_NA -QFMT=fastap -SUPFIX=0119_BZ50.rnI -MINMATCH=0.1
-LOOPEXT=0 -UNITG=bits -START=1 -END=-1 -MATRIX=coligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALICN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50
-USER=US10048046_GCGN 1 1_193 @runat_10012006_122939_24142 -NCPU=6 -ICPU=3
-NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPORTS=60 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scorting tables
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mezoe ozen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                             00000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otal number of hits satisfying
              44446769
                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic search,
                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_NA:*

1: /cgn2_6/ptodata/l/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/l/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/l/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/l/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/l/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/l/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/l/ina/PCOMB.seq:*

8: /cgn2_6/ptodata/l/ina/RB_COMB.seq:*

9: /cgn2_6/ptodata/l/ina/RB_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XGAPOD 60.0
YGAPOD 60.0
YGAPOD 6.0
PGAPOD 6.0
Delop 6.0
                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            January 12, 2006, 07:58:47 , Search time 316 Seconds (without alignments) 3735.130 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-048-046-2
664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1303057 ведв,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MERPEEGKQSPPPQPWGRLL.....VKAHHAMKFNHICEQTRFKN 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٠.
                                                                                                                                                                                                              멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xgapext
Ygapext
Fgapext
Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $
                     US-09-396-196G-104092

US-09-396-196G-104100

US-09-396-196G-104101

US-09-396-196G-104102

US-09-396-196G-104103

US-08-078-35

US-08-471-970A-35

US-08-471-970A-35

US-08-471-970A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chosen parameters:
                                                                                                                                                                                                            片
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bummaries
                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0
7.0
7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1293591
Sequence 104092,
Sequence 104101,
Sequence 104101,
Sequence 104103,
Sequence 104103,
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 16, Appl
                                                                                                                                                                                                          Description
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-09-396-196G-104092/c
~~~~nce 104092_Application US/09396196G
                                                                                                                                                                                                                                      APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                             Alignment Scores:
                                                                                                                             US-09-396-196G-104092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000000000000000000000
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 127806
SOPTWARE: PastSEQ for Windows Version
SEQ ID NO 104092
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 104092, App
Patent No. 6821724
GENERAL INFORMATION:
                                                                                                                                            ORGANISM: mus musculus
                                                                                                                                                           TYPE: DNA
                                                                                                                                                                           LENGTH:
                                                                               No::
                                                                                                                                                                            25
           148
7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-582-740-6
US-08-582-740-6
US-09-109-879-63
US-09-109-879-63
US-09-131-473B-77
US-07-931-473B-77
US-07-714-131C-77
US-08-421-110-179
US-08-412-110-179
US-08-412-110-179
US-08-412-110-179
US-08-469-609A-77
US-08-469-609A-77
US-08-469-609A-77
US-08-469-609A-77
US-08-469-609A-109
US-09-143-190-77
US-09-143-190-77
US-09-143-190-77
US-09-143-190-77
US-09-143-190-77
US-09-143-190-77
US-09-143-190-77
US-09-143-190-77
US-09-143-190-77
US-09-143-190-79
US-09-143-190-79
US-09-143-190-79
US-09-143-190-79
US-09-143-190-79
US-09-143-190-79
US-09-143-190-79
US-09-143-190-79
US-09-311-486C-1141
US-09-350-275-31
US-09-350-275-31
US-09-350-275-31
US-09-350-275-31
US-09-350-275-31
US-09-350-275-31
US-09-350-275-31
US-09-350-275-31
US-08-964-725-12
US-08-964-725-12
US-08-964-725-12
US-08-964-725-12
US-08-964-725-12
US-08-964-725-12
US-08-964-725-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                            4.0
0000,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Appli
Sequence 63, Appli
Sequence 63, Appli
Sequence 77, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 77, Appl
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 109, Appl
Sequence 1074, Appl
Sequence 10937, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 31, Appl
Sequence 325, Appl
Sequence 25, Appl
Sequence 25, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
```

US-10-048-046-2

(1-664)

x US-09-396-196G-104092

(1-25)

```
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE; 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT ETLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 104100
TENCETH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
U8-10-048-046-2 (1-664) x U8-09-396-196G-104101 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U8-09-396-196G-104101/c
U8-09-396-196G-104101/_Application US/09396196G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-048-046-2 (1-664) x US-09-396-196G-104100 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-396-196G-104100/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104100
                                                                                                                                                                     ) ORGANISM: mus musculus
US-09-396-196G-104101
                                                                                                                                 Alignment Scores
                                                                                                                                                                                                                                   SOPTWARE: PASTSEQ for Windows Version 4.0 SEQ ID NO 104101
                                                                                                                                                                                                                                                                   APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REPERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
'CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ. ID NOS. 127806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Michael Mittmann APPLICANT: David Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 ArgLeuLeuArgLeuGlyAla 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATTGCTCAGATTGGGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATTGCTCAGATTGGGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                            David Lockhart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         David Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09396196G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
1.05%
                                                148
7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.00
                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                     0000
```

```
RESULT 4
US-09-396-196G-104102/c
~~~~~~~ 104102, Application US/09396196G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             묽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-046-2 (1-664) x US-09-396-196G-104102 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-396-196G-104103/c
                                                                                                                             US-09-396-196G-104103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-396-196G-104102
          Query Match:
                                                           score:
                                                                                          Alignment Scores:
                                                                             Pred. No.:
                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104103
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 104102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6821724
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 104103, Patent No. 682172
                                                                                                                                                                                                                                                                       APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1299-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
CURRENT FILING DATE: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                              ORGANISM: mus musculus
                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 ArgieuleuArgieuGlyAla 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATTGCTCAGATTGGGCGCT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATTGCTCAGATTGGGCGCT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09396196G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
1.05%
1.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.00
                             100.00%
                                                             7.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                             Length:
Matches:
                             Conservative:
Mismatches:
                 Indels:
 000042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000048
```

```
ঠ
                                                                                                                                US-08-471-970A-35/c
                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                 US-10-048-046-2 (1-664) x US-08-078-683A-35 (1-30)
                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-078-683A-35/c
                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     융
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U8-10-048-046-2 (1-664) x U8-09-396-196G-104103 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                    18-08-078-683A-35
                                                                                               Sequence 35, Application US/08471970A Patent No. 6531295
                                GENERAL INFORMATION:
APPLICANT: Saundes
APPLICANT: Bernfie
APPLICANT: Kato, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 35;
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CME-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: U9/08/078,683A
FILING DATE: 17-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                     8
0
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKPIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Kato, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IITLE OF INVENTION: Construction and USe of Synthetic IITLE OF INVENTION: Constructs Encoding Syndecan NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U. ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                  623 SerGluLeuProValAlaVal 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 ArgieuleuArgieuGlyAla 24
               T: Saunders, Scott
T: Bernfield, Merton
T: Kato, Masato
INVENTION: Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lication US/08078683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eingle
                                                                                                                                                                                                                                                                                       100.00%
100.00%
1.05%
Construction and USe of Synthetic Constructs Encoding Syndecan
                                                                                                                                                                                                                                                                                                                                                  00
                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                    Conservative:
                                                                                                                                                                                                                                                                                  000078
```

```
RESULT 8
US-09-723-677B-35/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-048-046-2 (1-664) x US-08-471-970A-35 (1-30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-471-970A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPB: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/09723677B Patent No. 6699968
                                                    TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN FILE REFERENCE: 101553-151

CURRENT REPLICATION NUMBER: US/09/723,677B

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 08/471,970

PRIOR PILING DATE: 1995-06-06

PRIOR PILING DATE: 1995-06-06

PRIOR PILING DATE: 1993-06-17

PRIOR APPLICATION NUMBER: 08/078,683

PRIOR PILING DATE: 1993-06-17

PRIOR APPLICATION NUMBER: 07/856,869

PRIOR PILING DATE: 1993-08-06

PRIOR PILING DATE: 1992-08-06

PRIOR PILING DATE: 1992-08-06

PRIOR PILING DATE: 1992-09-06

PRIOR PILING DATE: 1992-09-06

PRIOR PILING DATE: 1992-09-06

PRIOR PILING DATE: 1992-09-06
                                                                                                                                                                                                                                                                                                             APPLICANT: SAUNDERS, SCO.
APPLICANT: BERNPIELD, MI
APPLICANT: KATO, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/
PILING DATE: 17-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: P-41,10
REFERENCE/DOCKET NUMBER: CMI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2. STREET: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                 APPLICATION NUMBER: 07/746,797
FILING DATE: 1991-08-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    623 SerGluLeuProValAlaVal 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 receaerreceerrecaere 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
NUMBER: 07/331,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                           SCOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.05%
                                                                                                                                                                                                                                                                                                                                       MERTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/078,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/471,970A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-41, 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMB-062DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000073
```

```
PRIOR FILING DATE: 1989-03-29
INUMBER OF SEQ ID NOS: 46
SOFTWARE: PACENTIN VERSION 3.0
SEQ ID NO 35
LENGTH; 30
TYPE: DNA
CRGANISM: MUS SP
US-09-723-677B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-048-046-2 (1-664) x US-09-723-677B-35 (1-30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-196-538-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                             Pred. No.:
                                                                              Alignment Scores:
                                                                                                              US-08-196-538-16
                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 33
LENGTH: 33
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 563960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stanley Tabor
APPLICANT: Charles C. Richardson
TITLE OF INVENTION: USE OF SHORT OLIGONUCLEOTIDES AS PRIMERS
TITLE OF INVENTION: FOR DNA SEQUENCING
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/985
PILING DATE: December 13,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOSTWARE, Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Callar
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/196,538 FILING DATE: Pebruary 14, 1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY
                                                                                                                                                                                                                                     TELBPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         623 SerGluLeuProValAlaVal 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 TCCGAGTTGCCGGTTGCAGTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08196538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                    (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
                193
7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.00
                                                                                                                                                                                                                                                                                                                                                 07/985,468
ber 13, 1992
                                                                                                                                                                                                                                                                                     206/090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000073
                     0073
高海 医睫状束形成的 医路动物
```

```
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-048-046-2 (1-664) x US-08-196-538-16 (1-33)
                                                                                                                                  RESULT 11
US-09-109-879-6
                                                                                                                                                                                            문
                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                   US-10-048-046-2 (1-664) x US-08-582-740-6 (1-35)
                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-582-740-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-582-740-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08582740
Patent No. 6037324
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: Inhibitors of MACCAM-1-Mediated
TITLE OF INVENTION: Interactions and Methods of Use Therefor
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/582,740
FILING DATE: 04-JAN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BTOOK, DAVID E.
REGISTRATION NUMBER: 12,592
REFERENCE/DOCKET NUMBER: 12595-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
Sequence 6, Application US/09109879

Patent No. 6274556

GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Schwender, Charles F.
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MACCAM-1-MEDIATED
TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 ProArgValProProSerSer 165
                                                                                                                                                                                                                          207 GlyserGlyGlyGlyGlyIle 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CCGAGAGTTCCACCTTCCTCG 26
                                                                                                                                                                                              7
                                                                                                                 Application US/09109879
                                                                                                                                                                                            GGATCCGGTGGAGGAGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1:05%
2
                                                                                                                                                                                                                                                                                                                         7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6:
                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
Gaps:
                                                                                                                                                                                                                                                                                                             0000735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00
```

THEREFOR

#1.30

```
RESULT 12
US-08-582-740-63/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-048-046-2 (1-664) x US-09-109-879-6 (1-35)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acore:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-109-879-6
                                                                                                                                                                                                                           Sequence 63, Application US/08582740
Patent No. 6037324
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Schwender, Charles F.
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: Inhibitors of MAdCAM-1-Mediated
TITLE OF INVENTION: Interactions and Methods of Use Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: (781) 861-954 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC computer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US97/00291
PILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/582,740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                         NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 04-JAN-1996
ATTORNBY/AGENT INFORMATION:
NAME: Brook, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: 02-JUL-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8: CORRESPONDENCE ADDRESS:
MEDIUM TYPB: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         STREET: Two Militia I CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/109,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSES: Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                           DDRESSES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BNGTH: 35 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GlyserGlyGlyGlyGlyIle 213
                                                                                                                                                                                                                                                                                                                                                                                                                            7. GGATCCGGTGGAGGAGGAATT 27
                                                                             02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two Militia Drive
                                                                                                                                                   Two Militia Drive
                                                                                               USA
                                                                                                                                                                   Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.05
                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKS95-12A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0000735
```

유 ঠ

```
US-09-109-879-63/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-048-046-2 (1-664) x US-08-582-740-63 (1-39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-582-740-63
                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/109,879
FILING DATE: 02-UUL-1998
CLASSIFICATION STA
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00291
APPLICATION NUMBER: PCT/US97/00291
FILING DATE: 03-UAN-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/582,740
FILING DATE: 04-UAN-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION TOPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/09109879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      STREET: LANCE CITY: Lexington CITY: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: INTITLE OF INVENTION: INTITLE OF INVENTION: INTITLE OF SEQUENCES: 85 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Brook, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,740
FILING DATE: 04-JAN-1996
                 NAME: Brook, David REGISTRATION NUMBER:
 REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAMB/KBY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 GlySerGlyGlyGlyGlyIle 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                     David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INHIBITORS OF MACCAM-1-MEDIATED INTERACTIONS AND METHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63:
LKS95-12A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000046
```

```
NAMB/KEY:
LOCATION:
US-09-109-879-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
U8-07-931-473B-77/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-048-046-2 (1-664) x US-09-109-879-63 (1-39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
Percent Similarity:
                Score
                                Pred. No.:
                                               Alignment Scores:
                                                                              JS-07-931-473B-77
                                                                                           TELEPAX: (303) 850-9401
INFORMATION FOR SEG ID NO: 77:
BEQUENCE CHARACTERISTICS:
LENGTH: 40 nucleotides
TYPE: NUCLEIC ACID
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 77, Application US/07931473B Patent No. 5270163
                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 1920817
CLASSIFFCATION: 435
PRIOR APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPAX: (303) 850-9900
TELEPAX: (303) 850-9901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: (781) 861-9540 INFORMATION FOR 8EQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Larry Gold APPLICANT: Craig Tuerk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET; COLORADO USA
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 15..
COMPUTER: 15..
OPERATING SYSTEM: M5-10.
OPERATING WordPerfect 5.1
OPERATING MORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 80237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLE OF INVENTION: Nucleic Acid Ligands
MBER OF SEQUENCES: 335
RRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESSEB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 GlyserGlyGlyGlyGlyIle 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 GGATCCGGTGGAGGAGGAATT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Beaton & Swanson, P.C.
4582 South Ulster Street Parkway, #403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
 232
7.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63:
                                                                                                                                                                                                                                                                                                                                                                                                                             5.25 inch, 360 Kb storage
 Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000078
    076
```

```
문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-048-046-2 (1-664) x US-07-931-473B-77 (1-40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                           ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-931-473B-109/c
                                                              US-10-048-046-2 (1-664) x US-07-931-473B-109 (1-40)
                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 109, Application US/07931473B
Patent No: 5270163
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Mucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MOOTDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 19920817
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850.9900
                                                                                                                                                                                                                                                                                          TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 nucleotides
                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 ProSerThrSerValSerLeu 467
                            461 ProSerThrSerValSerLeu 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 CCTTCGACATCCGTGAGCTTG 2
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3B: Beaton & Swanson, P.C.
4582 South Ulster Street Parkway, #403
                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
1.05%
                                                                                                            232
7.00
100.00%
100.00%
1.05%
                                                                                                                                                                                                                                                                                                                                109:
                                                                                                                                                              Length:
Matches:
                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kb storage
                                                                                                  000076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             000
```

Search completed: January 12, 2006, 10:59:56 Job time : 317 secs

```
Regult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-O=/cgn2 1/USPTO spool/US10048046/runat 10012006 122940 24178/app_query.fasta_1.839
-DB=PublIshed_Applications NA Main -QFMT=fastap -SUFFIX=011g_sz50.rmpbm
-MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -UNITS-blts -START=1 -END=-1 -MATRIX=011go
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=50
-USER=US10048046 @CGN 1 1 1026 @runat 10012006 122940 24178 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEGESCONES=0 -WAIT -DSPBECK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           schringatablen, object
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U8-10-048-046-2
664
1 MERPEEGKQSPPPQPWGRLL.....VKAHHAMKFNHICEQTRPKN 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                January 12, 2006, 10:50:02; Search time 1360 Seconds (without alignments) 4037.402 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA_Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9793542 seqs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xgapop 60.0 , Xgapext 60.0
Ygapop 60:0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                             / (cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ (cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyright
                                                                                                                                                                                                                  Length
     GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                       멂
     555555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chosen parameters:
US-11-036-317-24394

US-11-036-317-60227

US-11-036-317-61246

US-11-036-317-61892

US-11-036-317-131760
                                                                                                                                                                                                                    ㅂ
                                                                                                                                         US-10-719-956-88030
US-11-036-317-24277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bummaries
                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11076785
                                        Sequence 88030, A
Sequence 24277, A
Sequence 24394, A
Sequence 60227, A
Sequence 61246, A
Sequence 67592, A
                                                                                                                                                                                                               Description
  Sequence
```

000 0000	0.0	
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	366433333333333	110 110 110 110 110 110 110 110 110 110
•		
,		
	. ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	
ــر مر مر مر مر مر مر - د د د د د د د د د د د د د د د د د د د		
	, , , , , , , , , , , , , , , , , , , ,	
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
		ហេសសហសេសសេសសេសសេសសេស
	0000000	000000000000000000000000000000000000000
US-1 US-1 US-1 US-1 US-1 US-1		
0-71		
119-9 119-9 19-9 19-9 19-9	### ### ############################	00000000000000000
00000000000000000000000000000000000000	00000000000000000000000000000000000000	7777773333333333
3114498361 3114498361		
999 999 292 012	460000446 401 40000446 401	92365444400093034610000000000000000000000000000000000
	មាស្តាល្ចប់	ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο
2000 2000 2000 2000 2000 2000 2000 200		
equenc equenc equenc equenc equenc equenc	sequence sequence sequence sequence sequence sequence equence	equence control of the control of th
••••••••		
0 2 2 4 4 4 8 0 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1844 2033 2039 2039 2223 2223 2256 2364 2791 1049 1049 1050	144 153 153 153 153 153 153 153 153 153
1, Ap 9, Ap 5, Ap 91, A 92, 12,	752555	40640648664866
PO-0-9-P	>>6 x x x x x x x x x x x x x x x x x x	```>>>

ALIGNMENTS

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
FIILE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1
SEQ ID NO 88030 ৪ US-10-048-046-2 (1-664) x US-10-719-956-88030 (1-25) Query Match: Percent Similarity: Best Local Similarity: Score: Pred. No.: Alignment Scores: US-10-719-956-88030 RESULT 1 US-10-719-956-88030 Sequence 88030, Application US/10719956 Publication No. US20040146910A1 TYPE: DNA CREATING CONTROL ORGANISM: Rattus norvegicus LENGTH: 25 303 ThrCysIleIleCysGlnAspLeu 310 9.00 100.00% 100.00% 1.20% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 000087

```
용
                                                              ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-11-036-317-24394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Mus musculus
US-11-036-317-24277
                                                                                                  US-10-048-046-2 (1-664) x US-11-036-317-24394 (1-25)
                                                                                                                                                     Query Match:
                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                      ) ORGANISM: Mus musculus
US-11-036-317-24394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bequence 24277, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT FILING DATE: 2005-01-13

CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24394, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 24277
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF 5EQ ID NOS: 991174
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
18Q ID NO 24394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Williams, Alan
APPLICANT: Blums, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                                                                                       .
0
:
                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 LeuserPheProserAsnLysLeu 55
                                                                                                                                                                                                                                                                                                                          N
U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTCTTTCCCCAGCAATAAACTG 24
                                                                  SerPheProSerAsnLysLeuVal 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
8.00
100.00%
100.00%
                                                                                                                                                   72
8.00
100.00%
100.00%
                                                                                                                                                     Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000088
                                                                                                                                      ၀၀၀၀ဗ႘
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-60227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-036-317-60227
                                  ફ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                           US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)
                                                                                                                                   Query Match:
                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-61246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-036-317-61246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61246, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
APPLICANT: Blume, John
FITTLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 60227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60227, Application US/11036317 Publication No. US20050214823A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blume, John TITLE OF ANALYBIS OF Alternative Splicing in Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Williams, Alan APPLICANT: Blume, John
                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 SerPheProSerAsnLysLeuVal 56
                          47. AspLeuSerPheProSerAsnLys 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTTTCCCCAGCAATAAACTGGTC 24
N
  GACCTCTCTTTCCCCCAGCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.00
100.00%
100.00%
                                                                                                                                     100.00%
100.00%
1.20%
                                                                                                                                                                                                8.00
  25
                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                         Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ၀၀၀၀ಱည္ဟ
```

US-11-036-317-67592

Sequence 67592, Application US/11036317 Publication No. US20050214823A1

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                        US-11-036-317-131760
                                                                                                           RESULT 8
                                                                                                                                                                                                              US-10-048-046-2 (1-664) x US-11-036-317-108822 (1-25)
                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Mus musculus US-11-036-317-108822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-036-317-108822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-046-2 (1-664) x US-11-036-317-67592 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Mus musculus
US-11-036-317-67592
Sequence 131760, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 108822
LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 108822, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blums, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
PILE REPERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 67592
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                 388
                                                                                                                                               1 GATATGCTGCAACCCAAAGTCAGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                    AspMetLeuGlnProLysValArg 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysAspLeuSerPheProSerAsn 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGACCTCTCTTTCCCCAGCAAT 24
                                                                                                                                                                                                                                                                  100.00%
                                                                                                                                                                                                                                                                                                                         72
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matchee:
                                                                                                                                                                                                                                                   000088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဝဝဝဝစ္မ
```

```
RESULT 10
US-11-036-317-153103
                                                                                                                                                                                                                                                                                               US-10-048-046-2 (1-664) x US-11-036-317-144618
                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-036-317-144618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-048-046-2 (1-664) x US-11-036-317-131760 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-036-317-144618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-036-317-131760
                                                    Sequence 153103, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
APPLICANT: Blume, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 144618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 144618, Application US/11036317
publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
CURRENT APPLICATION NUMBER: US/11/036,317
                APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing
FILE REFERENCE 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 131760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Method of Analysis of Alternative Splicing FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microarray Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 25
                                                                                                                                                                                                                                                            413 AspValAspSerGluSerSerAsp 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 MetProAspArgArgAlaGluArg 499
                                                                                                                                                                                                                    2 GATGTCGACAGTGAATCCTCAGAT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ATGCCTGACCGGAGAGCTGAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-01-13
                                                                                                                                                                                                                                                                                                                                                         8.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
8.00
100.00%
100.00%
1.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                               Conservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                   (1-25)
                                                                                                                                                                                                                                                                                                                                         000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse
```

CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13

```
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ঠ
                                                                                                                                                                                                                                                                                    გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-048-046-2 (1-664) x US-11-036-317-153103 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus US-11-036-317-153103
                                                                                                                                                                                                                                                                                                                          US-10-048-046-2 (1-664) x US-11-036-317-166836 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          j ORGANISM: Mus musculus
US-11-036-317-166836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U8-11-036-317-166836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 166936, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 153103
LENGTH: 25
                                                                                                                                            Sequence 198348, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Wethod of Analysis of Alternative
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Wethod of Analysis of Alternative
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                    -11-036-317-198348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 166836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 SerGluAspleuLeuGluLeuSer 412
                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TCAGAGGACCTGCTAGAGCTGTCT 25
                                                                                                                                                                                                                                                        ພ
                                                                                                                                                                                                                                                        AGGAGGAGAGGCTGTGACCTCTCT 25
                                                                                                                                                                                                                                                                                     ArgArgArgGlyCysAspLeuSer 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
8.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                              8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ၀၀၀၀စမ္ဟ
                                                                                                                                                                                                                                                                                                                                                                 000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Splicing in Mouse
                                                                                              Splicing
                                                                                              in Mouse
```

11.1·1 日上安林田一衛衛之下

```
Sequence 259770, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US.60/536,639

PRIOR PILING DATE: 2004-01-13

NUMBER: OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 259770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus 
US-11-036-317-198348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                     US-10-048-046-2 (1-664) x US-11-036-317-233307
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-048-046-2 (1-664) x US-11-036-317-198348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                              US-11-036-317-259770
                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Mus musculus 
US-11-036-317-233307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-036-317-233307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 198348
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS; 991174
SOFTWARE; Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 233307
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 233307, Application US/11036317 Publication No. US20050214823A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                       559 IleLeulysAsnTyrLeuAlaThr 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                                                                                                                                                                                                                                     2 ATCCTGAAGAATTACCTGGCAACC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgArgArgGlyCysAspLeuSer 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
1.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .72
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                            (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000082
                                                                                                                                                                                                                                                                                                                                                                                                                                  ၀၀၀၀စမ္ဟ
                                                                                                                                                        Splicing in
                                                                                                                                                          Mouse
```

```
RESULT 15
US-11-036-317-289125
(Sequence 289125, Application US/11036317
(Sequence 289125, Application US/11036317
(Publication No. US20050214823A1
(GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
(CURRENT FILING DATE: 2005-01-13
(CURRENT FILING DATE: 2005-01-13
(PRIOR APPLICATION NUMBER: US/11/036,317
(FILING DATE: 2004-01-13
(NUMBER OF SEQ ID NOS: 991174
(SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
(SEQ ID NO 289125
(TYPE: DNA
(ORGANISM: Mus musculus)
Search completed: January 12, 2006, 13:54:49
Job time : 1361 sece
                                                                                         გ
                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ঠ
                                                                                                                     US-10-048-046-2 (1-664) x US-11-036-317-289125 (1-25)
                                                                                                                                                                                                                                  Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-048-046-2 (1-664) x US-11-036-317-259770 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-259770
                                                                                                                                                                                                                     Score:
                                                                              558 AspileLeuLysAsnTyrLeuAla 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 GlyArgArgArgGlyCysAspLeu 48
                                                         1 GACATCCTGAAGAATTACCTGGCA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGAAGGAGGAGGCTGTGACCTC 25
                                                                                                                                                     72
8.00
100.00%
100.00%
1.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative: Mismatches: Indels: Gaps:
                                                                                                                                                                                                  Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                000088
                                                                                                                                                     000000
```

```
Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10048046/runat_10012006_122941_24202/app_query.fasta_1.839
-Q=/cgn2_1/USPTO_spool/US10048046/runat_10012006_122941_24202/app_query.fasta_1.839
-DB=Publiahed_Applications_NA_New -QFMT=fastap -SUFFIX=01ig_8z50.rupbn
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01igo
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -TRR SCORE=quality -THR_MIN=1
-ALIGN=15 -MODEL-COAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50
-USER=US10048046 @CGN 1 1_220 @runat_10012006_122941_24202 -NCPU=6 -ICPU=3
-NO_MMAP -LARGROUTHY -NEG_SCORES=0 -WAIT -DBFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The state of the s
                                                                                                                                                                                                                                                                                                                                                                                                                      Regult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scotling Cabber Coluce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Meximum DB seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                  o o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score greater than or equal to the score of the result beir and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1987654321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_NA_New:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      January 12, 2006, 10:56:48 ; Search time 294 Seconds (without alignments) 1827.916 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Pgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MERPEEGKQSPPPQPWGRLL.....VKAHHAMKFNHICEQTRFKN 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-046-2
664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6038814 seqs, 404674181 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
/cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
/cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/pubpna/US60_NEW
                                                                                                                                                                                                                                                                                                                                                                                                                           멾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $
US-10-310-914A-42895

US-10-310-914A-638790

US-10-310-914A-1320691

US-10-310-914A-520691

US-10-310-914A-574833

US-10-310-914A-626661

US-10-310-914A-1064918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                   Sequence 638790,
Sequence 814306,
Sequence 1320691,
                                               Sequence
                                                                                                   Sequence
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                        Sequence 42895, A
         Sequence
                                                                                         e 1320691,
e 56004, A
e 374833,
                                                        626661,
```

9 7 1.1 22 6 US-10-310-914A-1205143 Sequence 1205143, 11 23 6 US-10-310-914A-42390 Sequence 37481, 23 6 US-10-310-914A-483394 Sequence 37481, 23 6 US-10-310-914A-483394 Sequence 482294, 23 7 1.1 23 6 US-10-310-914A-543344 Sequence 542344, 23 6 US-10-310-914A-133456 Sequence 1320692, 24 7 1.1 23 6 US-10-310-914A-133456 Sequence 1320692, 24 7 1.1 24 6 US-10-310-914A-133456 Sequence 1363456, 25 1.1 24 6 US-10-310-914A-1363456 Sequence 1363456, 27 1.1 24 6 US-10-310-914A-1363456 Sequence 1363456, 27 1.1 25 6 US-10-310-914A-1363451 Sequence 1363459, 27 1.1 25 7 US-11-121-849-321027 Sequence 222932, 28 1.1 25 7 US-11-121-849-321027 Sequence 232942, 27 1.1 25 7 US-11-121-849-321027 Sequence 232950, 27 1.1 25 7 US-11-121-849-321027 Sequence 321028, 27 1.1 25 7 US-11-121-849-321029 Sequence 321028, 27 1.1 25 7 US-11-121-849-321029 Sequence 321028, 27 1.1 25 7 US-11-121-849-421094 Sequence 321028, 27 1.1 25 7 US-11-121-849-421094 Sequence 321028, 27 1.1 25 7 US-11-121-849-421094 Sequence 321028, 28 1.1 25 7 US-11-121-849-421094 Sequence 321028, 28 1.1 25 7 US-11-121-849-421094 Sequence 321029, 28 1.1 25 7 US-11-121-849-421094 Sequence 321029, 38 1.1 25 7 US-11-121-849-421094 Sequence 321029, 38 1.1 25 7 US-11-121-849-421094 Sequence 321029, 38 1.1 25 7 US-11-121-849-421094 Sequence 321029, 39 1.1 25 7 US-11-121-849-421094 Sequence 321029, 30 1.1 25 7 US-11-121-849-4210		a				a		a			a		n			ဂ	Ω					a	a			a		a		n	o	a	o	a				a
1.1 22 6 US-10-310-914A-1205143 Sequence 1205143 1.1 23 6 US-10-310-914A-374831 1.1 23 6 US-10-310-914A-374831 1.1 23 6 US-10-310-914A-482394 1.1 23 6 US-10-310-914A-815510 1.1 23 6 US-10-310-914A-815510 1.1 23 6 US-10-310-914A-1320692 1.1 23 6 US-10-310-914A-136345 1.1 24 6 US-10-310-914A-136345 1.1 24 6 US-10-310-914A-126725 1.1 24 6 US-10-310-914A-126725 1.1 24 6 US-10-310-914A-126721 1.1 24 6 US-10-310-914A-126721 1.1 24 6 US-10-310-914A-126721 1.1 24 6 US-10-310-914A-22932 1.1 25 6 US-10-310-914A-22932 1.1 26 6 US-10-310-914A-22932 1.1 27 6 US-10-310-914A-22932 1.1 28 6 US-10-310-914A-363461 1.1 29 6 US-10-310-914A-363461 1.1 29 6 US-10-310-914A-363461 1.1 29 6 US-10-310-914A-363461 1.1 29 6 US-10-310-914A-363461 1.1 22 6 US-10-310-914A-36346 1.1 22 6 US-10-310-914A-36346 1.1 22 6 US-10-310-914A-36346 1.1 22 7 US-11-121-849-321027 1.1 22 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		45	44	43	42		40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	ø
1 22 6 US-10-310-914A-1205143 Sequence 1205143 1 23 6 US-10-310-914A-42890 Sequence 374831, 123 6 US-10-310-914A-482394 Sequence 374831, 123 6 US-10-310-914A-542344 Sequence 42394, 123 6 US-10-310-914A-1320692 Sequence 1320692 Sequence 1206925 Sequence 120694 Sequence 120695 Sequence 120694 Sequence 120695 Sequence 120694 Sequence 120695 Sequence 120694 Sequence 120695 Sequence 120694 Sequence 120695 Sequence 12		თ	o	o,	o	7	7	7 .	7	7.	7	7	7	. 7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
6 US-10-310-914A-1205143 Sequence 1205143 6 US-10-310-914A-42890 Sequence 374831, 6 US-10-310-914A-48234 Sequence 374831, 6 US-10-310-914A-61534 Sequence 374834, 6 US-10-310-914A-61534 Sequence 815304, 6 US-10-310-914A-136345 Sequence 1320692 Sequence 1320692 Sequence 1206925 S		0.9	0.9	٠	•		•	•	1.1	1.1	1.1	1.1.	1.1	1.1	•	•	•	•	•	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1	1.1
US-10-310-914A-1205143 Sequence 1205143 US-10-310-914A-48890 Sequence 42890, US-10-310-914A-48831 Sequence 42890, US-10-310-914A-18334 Sequence 812394, US-10-310-914A-123642 Sequence 1320692 US-10-310-914A-1320692 Sequence 1363465 US-10-310-914A-136345 Sequence 1363465 US-10-310-914A-1267239 Sequence 1060225 US-10-310-914A-1267239 Sequence 1288181 US-10-310-914A-1267239 Sequence 1288181 US-10-310-914A-1267239 Sequence 22932, US-10-310-914A-527609 Sequence 22932, US-10-310-914A-1363450 Sequence 22932, US-10-310-914A-1363450 Sequence 22932, US-10-310-914A-1363450 Sequence 22932, US-11-121-849-321027 Sequence 331027, US-11-121-849-321027 Sequence 321028, US-11-121-849-321029 Sequence 321028, US-11-121-849-428098 Sequence 321028, US-11-121-849-428098 Sequence 428099, US-11-121-849-428098 Sequence 1004394 US-10-310-914A-1004294 Sequence 1004294 US-10-310-914A-13635 Sequence 1004294 US-10-310-914A-13639 Sequence 17619, US-10-310-914A-13639 Sequence 17619, US-10-310-914A-1368 Sequence 17619, US-10-310-914A-89188 Sequence 17818, US-10-310-914A-19673 Sequence 176973, AllGNMFNTS							•	:						-																								
1205143 478931 4882394 4882394 815510 1320692 1320692 1363461 126821 1267239 1363461 1363461 1267239 1363461 1267239 1363461 1363461 1363461 1363461 1363461 1363666 14686666 15686666 17687369 1768735 1768735 1768735 1768735 1768735 1768735	ALIGNMENTS	US-10-310-	US-10-310-	US-10-310-	US-10-310-	US-10-939-	US-10-939-	US-10-939-	US-10-939-	US-10-310-914A-100429	US-10-310-914A-81579	US-10-310-914A-100430	US-11-121-	US-11-121-	US-11-121-	US-11-121-	US-11-121-	US-11-121-	S	SO	SD	SD	S	S	Sn	US-10-310	US-10-310	US-10-310	US-10-310	US-10-310	US-10-310	US-10-310-914A-132069	US-10-310-	US-10-310-	US-10-310-914A-48239	US-10-310-914A-37483	US-10-310-	US-10-310-
μ. σ									æ		w	w	w										Sequence	Sequence	Sequence	Sequence	Sequence							Φ	Sequence	Sequence	Seguence	Sequence
		176873,	144700,	•	•	•	•	•	•	v	•	u	568626,	428098,	428097,	421694,	415066,	321029,	321028,	321027,	239450,	1363459,	57609	222932,	97707, A	1363461,	1267239,	1128181,	1060225,	838918,	1363456,	1320692,	815510,	542344,	9	31	890.	05143

ALIGNMENT

RESULT 1 US-10-310-914A-42895

Sequence 42895, Application US/10310914A Publication No. US20060003322A1

GENERAL INFORMATION:

```
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses th
```

```
RESULT 4
US-10-310-914A-1320691/c
/ Sequence 1320691, Application US/10310914A
                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                       ) TYPE: RNA
) ORGANISM: Human
US-10-310-914A-814306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-310-914A-814306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-048-046-2 (1-664) x US-10-310-914A-638790 (1-21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                               US-10-048-046-2 (1-664) x US-10-310-914A-814306 (1-21)
                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-10-310-914A-638790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 814306, Application US/10310914A Publication No. US2006000332ZRI CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 638790, Application US/10310914A
Publication No. US20060003322AI
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REPERENCE: 06087.0200.CFUS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bentwich, Isaac APPLICANT: Bhiler, Kvuzat TITLE OP INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OP INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS. 1:
SOPTWARE: PatentIn vers:
SEQ ID NO 814306
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER, US/10/3
CURRENT FILING DATE; 2002-12-065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 21
TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO 638790
ENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 LeuValAlaGlnProArgArg 279 V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 CTAGTGGCCCAGCCCCGCAGA 1
                                                                                                       Glyalaglyalaglyarggly 156
                                                                             GGUGCUGGUGCGGGCAGAGGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380
7.00
100.00%
100.00%
                                                                                                                                                                                      100.00%
100.00%
1.05%
                                                                                                                                                                                                                                                      380
7.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10/310,914A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000042
                                                                                                                                                                                      000072
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                        RESULT 6
US-10-310-914A-374833
                                                                                                                                                                                                                                                          US-10-048-046-2 (1-664) x US-10-310-914A-56004 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-56004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-310-914A-56004/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-048-046-2 (1-664) x US-10-310-914A-1320691 (1-21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCOIE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-310-914A-1320691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1320691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 56004, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
Sequence 374833, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kyuzat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 56004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US20060003322A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                495 ArgArgAlaGluArgGluGln 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ArgLeuGlYAlaGluGluGlY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AGGTTGGGGGGGGGAGGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380
7.00
100.00*
                                                                                                                                                                                                                                                                                                                      397
7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.05%
                                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
```

APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable

group of novel regulatory genes

```
LENGTH: 22
; TYPB: RNA
; ORGANISM: Human
US-10-310-914A-374833
                                                                                                                                                                                                                                                                                                   ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
APPLICANT: Bhiler, Kvuzat
ITITLE OF INVENTION: Beloinformatically detectable group of novel regulatory genes and
ITITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 626661
LENGTH: 22
TYPE: RAA
ORGANISM: Human
US-10-310-914A-626661
                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                 용
                                                                                                                                                                                                                                                                                                                                        US-10-048-046-2 (1-664) x US-10-310-914A-626661 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-310-914A-626661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-048-046-2 (1-664) x US-10-310-914A-374833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                               3-10-310-914A-1064918/c
Sequence 1064918, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 626661, Application US/10310914A Publication No. US/20060003322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8EQ ID NO 374833
           APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: uses thereof FILE REPERBNCE: 06087.0200.CPUS01 CURRENT EPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOPTMARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                     150 GlyAlaGlyAlaGlyArgGly 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 GlyalaGlyalaGlyargGly 156
                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGGCAGGGGCUGGGCGGGG
SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                                                                              397
7.00
100.00%
100.00%
1.05%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-22)
                                                                                        group
                                                                                                                                                                                                                                                                                                                                                                                000072
                                                                                      of novel regulatory
```

```
Sequence 42890, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable gro

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 42890
                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                       RESULT 10
US-10-310-914A-42890
                                                                                                                                                                                                                                                                                                                                                                                                US-10-048-046-2 (1-664) x US-10-310-914A-1205143
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-310-914A-1205143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-10-310-914A-1205143/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-048-046-2 (1-664) x US-10-310-914A-1064918 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-310-914A-1064918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1205143
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1205143, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: PatentIn version 3.3 SEQ ID NO 1064918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLS OF INVENTION: Bioinformatically detectable
TITLS OF INVENTION: Uses thereof
FILS REFERENCE: 06087,0200,CFUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
LENGTH: 23
TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                               156 GlyAlaAspProArgValPro 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 ArgValProProSerSerPro 166
                                                                                                                                                                                                                                                                                                                             21 GGAGCGGACCCTAGGGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                              group of novel regulatory genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group
                                                                                                                                                                                                                                                                                                                                                                                                                                      000072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of novel regulatory
```

genes

ORGANISM: Human

0000

and

```
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-10-310-914A-482394
                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                       ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-048-046-2 (1-664) x US-10-310-914A-374831 (1-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-048-046-2 (1-664)
 Score
                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-310-914A-374831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-310-914A-42890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                 US-10-310-914A-482394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-310-914A-374831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1380402
SOPTWARE: Patentin version 3.3
SEQ ID NO 374831
                                                                                                                                                                                                                                                                                                  Sequence 482394, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 374831, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                                                                 SEQ ID NO 482394
                                                                                                                                               APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzet
TITLE OF INVENTION: Bioinformatically detectable group
TITLE OF INVENTION: uses thereof
FILE-REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 23
TYPB: RNA
ORGANISM: Human
                                                                                 ORGANISM: Human
                                                                                                                   ENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
0
:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 GlyAlaGlyAlaGlyArgGly 156
                                                                                                                                                                                                                                                                                                                                                                                                                                150 GlyAlaGlyAlaGlyArgGly 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGGCAGGGGCUGGGCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414
7.00
100:00%
100.00%
1.05%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414
7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x US-10-310-914A-42890
7.00
                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000078
                                                                                                                                                                                                                                                        of novel regulatory genes and
                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-310-914A-542344/c

Sequence 542344, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shilar, Kvuzati

TITLE OF INVENTION: uses thereof

FITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087,0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOPTWARE: PALAL
                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-310-914A-815510/c
US-10-310-914A-815510/, Application US/10310914A
; Bequence 815510, Application US/10310914A
; GENERAL INFORMATION:
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-048-046-2 (1-664) x US-10-310-914A-542344 (1-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-048-046-2 (1-664) x US-10-310-914A-482394 (1-23)
                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                        US-10-310-914A-815510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-542344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 542344
                                                                                                                                                                                                                          SEQ ID NO 815510
                                                                                                                                                                                                                                    APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                      TYPE: RNA
                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 LeuPheProThrAlaSerAla 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 ArgieuleuArgieuGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 CIGITCCCCACAGCCAGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.05%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
                                   414
7.00
100.00%
100.00%
1.05%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative: Mismatches:
                                                     Mismatches:
                                                                      Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                       Indels:
```

-/'₄

000012

```
WS-10-310-914A-1320692/c
US-10-310-914A-1320692/c
| Sequence 1320692, Application US/10310914A
| Publication No. US20060003322A1
| Publication No. US20060003322A1
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
| TITLE OF INVENTION: Uses thereof
| FILE REFERENCE: 06087.0200.CPUS01
| CURRENT APPLICATION NUMBER: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 1320692
| LENGTH: 23
| TYPE: RUA
| ORGANISM: Human
| US-10-914A-1320692
Search completed: January 12, 2006, 13:59:49 Job time: 295 Becs
                                                                          밁
                                                                                                       ક
                                                                                                                                               US-10-048-046-2 (1-664) x US-10-310-914A-1320692 (1-23)
                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               문
                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U8-10-048-046-2 (1-664) x US-10-310-914A-815510 (1-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GlyAlaGlyAlaGlyArgGly 156
                                                                          23 CTANGGTTGGGGGCGGAGGAG 3
                                                                                                       20 LeuArgLeuGlyAlaGluGlu 26
                                                                                                                                                                                        414
7.00
100.00%
100.00%
1.05%
                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                        000012
```

ž,

ş

```
Title:
Perfect ecore:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring a cabic place of the cab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL-frame+ D2n.model -DEV=xlh
-MODEL-frame+ D2n.model -DEV=xlh
-MODEL-frame+ D2n.model -DEV=xlh
-MODEL-frame+ D2n.model -DEV=xlh
-MODEL-Green - Model -DEV=xlh
-De-PendIng Patents NA Main -QFMT=fastag -SUPFIX=011g_s250.rnpm -MINMATCH=0:1
-LOOPCIL=0 -LOOPEXT=0 -UNITS=bite -START=1 -RND=-1 -MATRIX=014g0
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=1
-ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50
-USER=US10048046 @GCGN 1 _7336 @runat 10012006 122940 24149 -NCPU=6 -ICPU=3
-NO MMAD -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -DELOY=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Messe 108(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-048-046-2
664
1 MBRPEEGKQSPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   January 12, 2006, 10:25:28 ; Search time 8980 Seconds (without alignments) 4088.375 Million cell updates/sec
                  Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/PCTUSA_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79147668 seqs, 27645789525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERPEEGKQSPPPQPWGRLL.....VKAHHAMKFNHICEQTRFKN 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
/cgm2 6/ptcdata/1/pna/PCTUSA_COMB.seq:*
/cgm2 6/ptcdata/1/pna/PCTUSC_COMB.seq:*
/cgm2 6/ptcdata/1/pna/PCTUSC_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO6_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO75_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO75_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO75_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO76_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO78_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO805_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO81_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO82_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO83_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO84_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO84_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO85_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO85_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO85_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO85_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO89_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO89_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO90_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO90_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO93_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO94_COMB.seq:*
/cgm2 6/ptcdata/1/pna/USO95A_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xgapext 60.0
Ygapext 60.0
Pgapext 7.0
Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87479736
```

```
``
Cgm2_6/ptodata/1/pna/US099C_COMB.seq:
Cgm2_6/ptodata/1/pna/US099C_COMB.seq:
Cgm2_6/ptodata/1/pna/US099C_COMB.seq:
Cgm2_6/ptodata/1/pna/US099C_COMB.seq:
Cgm2_6/ptodata/1/pna/US100B_COMB.seq:
Cgm2_6/ptodata/1/pna/US100B_COMB.seq:
Cgm2_6/ptodata/1/pna/US101C_COMB.seq:
Cgm2_6/ptodata/1/pna/US101C_COMB.seq:
Cgm2_6/ptodata/1/pna/US101A_COMB.seq:
Cgm2_6/ptodata/1/pna/US103B_COMB.seq:
Cgm2_6/ptodata/1/pna/US107B_COMB.seq:
Cgm2_6/ptodata/1/pna/US602B_COMB.seq:
Cgm2_6/ptodata/1/pna/US602B_COMB.seq:
Cgm2_6/ptodata/1/pna/US602B_COMB.seq:
Cgm2_6/ptodata/1/pna/US603_COMB.seq:
Cgm2_6/ptodata/1/pna/US604B_COMB.seq:
Cgm2_6/ptodata/1/pna/US604B_COMB.seq:
Cgm2_6/ptodata/1/pna/US604B_COMB.seq:
Cgm2_6/ptodata/1/pna/US604B_COMB.seq:
Cgm2_6/ptodata/1/pna/US604B_COMB.seq:
Cgm2_6/ptodata/1/pna/US604B_COMB.seq:
Cgm2_6/ptodata/1/pna/US604B_COMB.seq:
Cgm2_6/ptodata/1/pna/US605_COMB.seq:
Cgm2_6/ptodata/1/pna/US605_COMB.seq:
Cgm2_6/ptodata/1/pna/US605_COMB.seq:
Cgm2_6/ptodata/1/pna/US606_COMB.seq:
Cgm2_6/ptodata/1/pna/US606_COMB.seq:
Cgm2_6/ptodata/1/pna/US606_COMB.seq:
Cgm2_6/ptodata/1/pna/US606_COMB.seq:
Cg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cgn2_6/ptodata/1/pna/US096B_COMB.seq:
Cgn2_6/ptodata/1/pna/US096C_COMB.seq:
Cgn2_6/ptodata/1/pna/US097A_COMB.seq:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Regult No.	Score 8	Query Score Match Length DB		DB 37	ID US-09-953-570A-36815	Description Sequence 36815,
4444		, , , , , , , , , , , , , , , , , , ,		37 37 37	US-09-953-570A-36815 US-09-954-427A-238351 US-09-954-427A-238353 US-09-954-427A-238358	Sequence Sequence Sequence Sequence
, U		. 1.2	25	37	US-09-954-427A-238359	Sequence
ი ი 7 თ	& &	, , , , , ,	25 5	ა 8 8	US-09-956-604-29770 US-09-956-604A-29770	Sequence Sequence
ი 8	89	1.2	25	38	US-09-956-604B-29770	Sequence

```
Sequence 3615, Application US/09953570A

GENERAL INFORMATION:

APPLICANT: Mittmann, Michael

APPLICANT: Mittmann, Michael

FILE REFERENCE; 3110.1

CURRENT APPLICATION NUMBER: US/09/953,570A

CURRENT FILING DATE: 2001-09-13

PRIOR APPLICATION NUMBER: 60/232,638

PRIOR APPLICATION NUMBER: 60/232,638

PRIOR FILING DATE: 2000-09-14

NUMBER OF SEG ID NOS: 138410

NUMBER OF SEG ID NOS: 138410

SOFTWARE: Microarray Probe Sequence Listing Generat

SEG ID NO 36815
                                                                                                                                                                                                                                                                                                                                RESULT 1
US-09-953-570A-36815/c
                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Saccharomyces
US-09-953-570A-36815
                                          US-10-048-046-2 (1-664) x US-09-953-570A-36815
                                                                                                                               Alignment Scores:
                                                                                                                                                                                      LENGTH: 25
                                                                                                                      Хо.
:
 <u>د</u>
                     77
  ACCTCTACCAGTGGCACCGTGATT 1
                     ThreerThreerGlyThrValile 84
                                                                  716
8.00
100.00%
100.00%
1.20%
                                                                                                                                                                                                                                                                                                                                                                                                  cerevisiae
                                                                                                                                                                                                           Sequence Listing Generator V
                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                          Conservative: Mismatches: Indels:
                                                                                                          Length:
Matches:
                                           (1-25)
                                                                                                                                                                                                                                                                                      of Yeast
                                                                 000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
sequence
sequence
sequence
sequence
sequence
sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198348,
233307,
259770,
289125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62515
US-09-954-427A-238358, Application Sequence 238358, Application GENERAL INFORMATION:
APPLICANT: Michael Mittmann TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-954-427A-238353
; Sequence 238353, Application
; GENERAL INFORMATION;
; APPLICANT: Michael Mittmann
                                                       RESULT 4
                                                                            묽
                                                                                                S
                                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                                                                                       Score:
                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                               문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-238351
                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                 US-09-954-427A-238353
                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                SEQ ID NO 238353
LENGTH: 25
                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Rattus
                                                                                        302 LeuThrCysIleIleCysGlnAsp
                                                                              CTAACCTGTATCATCTGTCAAGAC
                                                                                                                                                                                                                                            Norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716
8.00
100.00%
100.00%
1.20%
                                                                                                                                             100.00%
100.00%
1.20%
                                                                                                                                                                                        .
8
                                   US/09954427A
  of Genetic Analysis of the
```

a

밁

ć. •

Rat

Genome

S

```
RESULT 2
US-09-954-427A-238351
US-09-954-427A-238351; Sequence 238351, Application US/09954427A
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
                                                                   US-10-048-046-2 (1-664) x US-09-954-427A-238353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-048-046-2 (1-664) x US-09-954-427A-238351 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/954,427A
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,166
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 420907
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 238351
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods of Genetic Analysis of the FILE REFERENCE: 3112.1 CURRENT APPLICATION NUMBER: U8/09/954,427A CURRENT FILING DATE: 2001-09-17 PRIOR APPLICATION NUMBER: 60/233,166 PRIOR FILING DATE: 2000-09-18 NUMBER OF SEQ ID NOS: 420907 SOPTMARE: Microarray Probe Sequence Listing Generator-V SOPTMARE: Microarray Probe Sequence Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 CysIleIleCysGlnAspLeuLeu 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGTATCATCTGTCAAGACCTTCTG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09954427A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
                                  309
                                                                                                                                                                                          Length:
Matches:
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
                                                                                                           Gара: ___
                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                     Generator-V 1.1
                                                                           (1-25)
                                                                                                                 ၀၀၀၀ಱ႘
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat Genome
```

```
밁
                                                                                                                                                                                                                                                                                                                ৪
                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                     US-10-048-046-2 (1-664) x US-09-954-427A-238359 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ક
                                                                                                                                                                                                                    US-09-956-604-29770/c
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-954-427A-238359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-954-427A-238359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UB-10-048-046-2 (1-664) x US-09-954-427A-238358 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rattus Norvegicus
US-09-954-427A-238358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/233,166
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 238359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                Sequence 29770, Application US/09956604
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
PILE REPERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILE REPERENCE: 3112.1
CURRENT APPLICATION NUMBER: US/09/954,427A
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,166
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 238358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 238359, App
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REPERENCE: 3112.1
CURRENT APPLICATION NUMBER: US/09/954,427A
CURRENT FILING DATE: 2001-09-17
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Michael Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Rattus Norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                    294 LysProAspLysMetGluGluThr 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 GluThrLeuThrCysIleIleCys 307
                                                                                                                                                                                                                                                                             2 AMACCAGACAAGATGGAGGAGACA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GAGACACTAACCTGTATCATCTGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09954427A
                                                                                                                                                                                                                                                                                                                                                                                                716
8.00
100.00%
100.00%
1.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                              Gape:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the Rat Genome
                                                                                                                                                                                                                                                                                                                                                                                              ဝဝဝဝစမ္က
```

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                          皮
                                                     US-09-956-604B-29770
                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-048-046-2 (1-664) x US-09-956-604A-29770 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ঠ
                                                                                                                                                                                                                                                                                                                                        US-09-956-604B-29770/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:

    TYPE: DNA
    ORGANISM: Escherichia coli
US-09-956-604-29770

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-956-604A-29770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-956-604A-29770/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-048-046-2 (1-664) x US-09-956-604-29770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                 Sequence 29770, Application US/09956604B

GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
FILE REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604B
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141659
SOUTWARE MICROGRAPH PROBE Sequence Listing Generator V 1.1
SEQ ID NO 29770
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/956,604A
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOPTWARE: Microarray Probe Sequence Listing Generator V
SEQ ID NO 29770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29770, Application US/09956604A
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 29770
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25
                                                                     ORGANISM: Bscherichia
                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                              462 SerThrSerValSerLeuThrThr 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 SerThrSerValSerLeuThrThr 469
                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AGTACGTCCGTATCGCTAACTACA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                          AGTACGTCCGTATCGCTAACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716
8.00
100.00%
100.00%
1.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.00
100.00%
100.00%
                                                                   coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000000
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : र्
                                                                                                                                                                                                                                              US-11-036-317-24277, Application US/11036317

Sequence 24277, Application US/11036317

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Slume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR PILING DATE: 2004-01-13

PRIOR FILING DATE: 2004-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ફ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-048-046-2 (1-664) x US-10-719-956-88030 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-719-956-88030
                                                                                                                                     ) ORGANISM: Mus musculus
US-11-036-317-24277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Rattus norvegicus
US-10-719-956-88030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-046-2 (1-664) x US-09-956-604B-29770 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멾
                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: U5/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarrey Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 24277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8EQ ID NO 88030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 88030, Application US/10719956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 25
                                                                                                                                                                                      LENGTH:
                                                                                    No.:
                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 ThrCysIleIleCysGlnAspLeu 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AGTACGTCCGTATCGCTAACTACA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerThrSerValSerLeuThrThr 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTGTATCATCTGTCAAGACCTT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            716
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.00
100.00%
100.00%
1.20%
               8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                 Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                   Indele:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
   ၀၀၀၀ಙ႘္ဟ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဝဝဝဝစမ္ဟ
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
                      S
                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus US-11-036-317-60227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-11-036-317-60227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-048-046-2 (1-664) x US-11-036-317-24394 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-24394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-036-317-24394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)
                                                         US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)
                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                       Sequence 60227, Application US/11036317

GENERAL INFORMATION:

APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OP INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2005-01-13

PRIOR FILING DATE: 2005-01-13

NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 991174.
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 24394
                                                                                                                                                                                                                                                                                                         SEQ ID NO 60227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                         ENGTH: 25
                        49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 LeuSerPheProSerAsnLysLeu 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TCTTTCCCCAGCAATAAACTGGTC
SerPheProSerAsnLysLeuVal 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerPheProSerAsnLysLeuVal 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application
                                                                                                             8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/11036317
                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                              0000825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000000
```

1.7 1.7 1.7 1.7 1.7

유

TCTTTCCCCAGCAATAAACTGGTC

```
RESULT 15
US-11-036-317-108822
, Sequence 108822, Application US/11036317
                                                                                                       ફ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                        유
                                                                                                                                            US-10-048-046-2 (1-664) x US-11-036-317-67592 (1-25)
                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                    Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                     ; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-67592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ફ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-036-317-67592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Mus musculus
US-11-036-317-61246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-036-317-61246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61246
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 991174

SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 67592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 61246, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
PRIOR PILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67592, Application US/11036317 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                         46 CysAspLeuSerPheProSerAsn 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 AspLeuSerPheProSerAsnLys 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GACCICICITICCCCAGCAATAAA 25
                                                                    TGTGACCTCTCTTTCCCCAGCAAT 24
                                                                                                                                                                                            8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.00
                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                               ၀၀၀၀စမ္ဟ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0000 B N
```

```
문
                              Ś
                                                               US-10-048-046-2 (1-664) x US-11-036-317-108822 (1-25)
                                                                                                               Query Match:
                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                   US-11-036-317-108822
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 108822
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILS REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                   TYPE: DNA
                  388 AspMetLeuGlnProLysValArg 395
1 GATATGCTGCAACCCAAAGTCAGG 24
                                                                                                  716
8.00
100.00%
100.00%
1.20%
                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                Gaps:
                                                                                                   0000 B N
```

Search completed: January 12, 2006, 13:29:43 Job time : 8982 secs

```
opino, peagranding
                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MODEL-frame+ p2n.model -DEV=xlh
-Q0-Cgn2 1/USPTO_spool/US10048046/runat_10012006_122940_24163/app_query.fasta_1.839
-Qs-Cgn2 1/USPTO_spool/US10048046/runat_10012006_122940_24163/app_query.fasta_1.839
-Qs-Cgn2 1/USPTO_spool/US10048046 = STPART=1 -END=-1 -MATRIX-oligo
-TCOPEXT=0 -UNITS-bite -STPART=1 -END=-1 -MATRIX-oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=1
-ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50
-USER-US10048046 @CGN 1 _78 @runat_10012006 122940_24163 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEGUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -DELOCK=100 -XGAPEXT=60 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                  Query
Score Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pending_Patents NA_New:*

1: /cgn2_6/ptcodata/1/pna/PCT_NEW_COMB.Beq:*

2: /cgn2_6/ptcodata/1/pna/US06_NEW_COMB.Beq:*

3: /cgn2_6/ptcodata/1/pna/US08_NEW_COMB.Beq:*

4: /cgn2_6/ptcodata/1/pna/US08_NEW_COMB.Beq:*

5: /cgn2_6/ptcodata/1/pna/US08_NEW_COMB.Beq:*

6: /cgn2_6/ptcodata/1/pna/US11_NEW_COMB.Beq:*

7: /cgn2_6/ptcodata/1/pna/US11_NEW_COMB.Beq:*

8: /cgn2_6/ptcodata/1/pna/US10_NEW_COMB.Beq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xgapop 60.0
Ygapop 60.0
Fgapop 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     January 12, 2006, 10:27:18 ; Search time 130 Seconds (without alignments) 2639.356 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-048-046-2
664
1 MERPEEGKQSPPPQPWGRLL......VKAHHAMKFNHICEQTRFKN 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1087749 ведв,
    0000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0
                                                2222221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xgapext 60.0
Ygapext 60.0
Pgapext 7.0
Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258370665 remidues
                US-10-562-561-867

US-10-527-552-18

US-10-527-552-18

US-11-294-621-70

US-11-317-798-5513

US-60-742-219-4800

US-11-130-6458-8449

US-11-130-6458-10537

US-11-130-6458-10712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chosen parameters:
                                                                                                                                                                                                                                                       Ħ
                                                                                                                                                                                                                                                                                                                          SUMMARIBS
                                    Sequence 562, App
Sequence 887, Appl
Sequence 18, Appl
Sequence 70, Appl
Sequence 5513, Ap
Sequence 4800, Ap
Sequence 8449, Ap
Sequence 10537, A
                                                                                                                                                                                                                                                       Description
Sequence
Sequence
```

									•															•••	••	••									
ť	Л	44	43	42	41	0	39	38	37	36	35	4	ü	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
d	h :	o	Ø	o	م	σ	σ	თ	o	σ	0	6	თ	o	თ	σ	6	თ	σ,	, 6	o	თ	Ō	on	്. ത	O	o,	Ø	σ	o,	o	თ	0	, O	o
	٠,		0.9	0.9	0:9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	.0.9	0.9	.0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	o. 9	0.9	0.9	0.9	0.9	0.9	0.9	0.9
7	3	4	<u>4</u> 2	41	41	41	41	39	38	35	35	35	35	34	34	33	31	. 30	30	30	29	27	26	25	25	25	25	25	25	25	25	23	22		22
-	J ·	7	σ	J	7	7	7	7	4	7	7	თ	ຫ	7	7	7	7	œ	œ	_	7	J	'n	æ	7	7	7	7	7	7	7	σ	7	7	7
05-71-00/-200-34	<u>.</u>	-11-067-260-71	US-10-199-820A-102	US-11-067-260-87	US-11-067-260-77	US-11-067-260-69	-11-067-260-	US-11-067-260-73	1-067-	US-11-317-798-5302	US-11-067-260-111	US-09-142-471D-13	US-09-142-471D-12	-11-317-798-3	-11-067-260-	-11-275-346-	US-11-262-284-10	-96	US-60-751-196-10	T-U805-1	-11-317-	-11-301-360-1	-10-149-553B-	-60-735-352-	-11-319-873-	-11-315-777-1	-11-067-260-9	-11-067-260-	9-09	-11-067-260-6	-11-067-260-	-10-515-051-7	-11-130-645B-	-11-130-645B-	US-11-130-645B-13924
sequence 3%, App		71	102,	e 87,	e 77,	e 69,	e 63,	73, 1	e 106	530	Sequence 111, App	13,	12,	367		N	10,	15,		e 2441,	e 554	107	37	12,	e H	e 	e 92,	e 67,	e 65	e 61,	e 59,	e 78,	e -	1392	Sequence 13924,
•	- 1		J	_	_	_	_	_	.0	·O	0	_	_	·o	_	,	_	_	,	σ'	σ,	0	_	_	,	-	_	_	_	_	_	_	×	⋗	23

ALIGNMENTS

RESULT 1 US-10-562-561-562/c

a

a

O

ი ი

0 0 0

```
| Sequence 562, Application US/10562561
| GENERAL INFORMATION: | APPLICANT: Siria Therapeutics, Inc. | APPLICANT: Siria Therapeutics, Inc. | APPLICANT: Bedgelman, Leonid | TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using TITLE OF INVENTION: Short Interfering Nucleic Acid (sinA) | FILIR REFERENCE: 400/166 (MEHB02-728-G) | CURRENT PILING DATE: 2005-12-28 | CURRENT PILING DATE: 2005-06-27 | CURRENT PILING DATE: 2003-06-27 | FRIOR APPLICATION NUMBER: US 10/60793 | FRIOR FILLING DATE: 2003-06-27 | FRIOR APPLICATION NUMBER: US 09/930423 | FRIOR APPLICATION NUMBER: PCT/US03/04710 | FRIOR APPLICATION NUMBER: US 09/930423 | FRIOR APPLICATION NUMBER: US 09/930423 | FRIOR APPLICATION NUMBER: US 10/205309 | FRIOR APPLICATION NUMBER: US 10/205309 | FRIOR APPLICATION NUMBER: US 10/720309 | FRIOR APPLICATION NUMBER: US 10/720448 | FRIOR APPLICATION NUMBER: US 10/757803 | FRIOR APPLICATION NUMBER: US 10/757803 | FRIOR APPLICATION NUMBER: US 10/757803 | FRIOR APPLICATION NUMBER: US 10/720448 | FRIOR APPLICATION NUMBER: US 10/633059 | FRIOR APPLICATION NUMBER: US 10/63
```

```
१
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-048-046-2 (1-664) x US-10-562-561-562 (1-19)
           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:
US-10-562-561-562
                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:
US-10-562-561-887
                                                                                                   Alignment Scores:
                                                                                                                                                                                                                            SOPTWARE: PatentIn
SEQ ID NO 887
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using TITLE OF INVENTION: Short Interfering Nucleic Acid (sina) FILE REFERENCE: 400/166 (MBHD02-788-G) CURRENT APPLICATION NUMBER: US/10/562,561 CURRENT FILING DATE: 2005-13-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 10/607933
PRIOR PILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 09/930423
PRIOR PILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: PCT/US03/04710
PRIOR PILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - NUMBER OF 8EQ ID NOS: 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 562
                                                                                     No.
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 10/693059
FILING DATE: 2003-10-23
APPLICATION NUMBER: US 10/444853
                                                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE: 2004-04-16
APPLICATION NUMBER: US 10/757803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 10/826966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 10/205309
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 10/720448 FILING DATE: 2003-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US04/16390 FILING DATE: 2004-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2004-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 ThrGluProSerProAla 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10562561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
              6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.00
            Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                    See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000006
0000619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Target Sequence/siNA sense
                                                                                                                                                             siNA antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-527-552-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-294-621-70/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 sergiyçiyçiyçiyile 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGGGAGGTGGAGGAATT 18
```

```
US-10-048-046-2 (1-664) x US-10-562-561-887
193 ThrGluProSerProAla 198
                                               (1-19)
```

APPLICANT: Sandoz GmbH
ITILE OF INVENTION: Process for production of
FILE REFERENCE: IB/G-32677A/BCK
CURRENT APPLICATION NUMBER: US/10/527,552
CURRENT FILING DATE: 2005-03-11
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 20
TYPE: NNA OTHER INFORMATION: oligonucleotide US-10-527-552-18 TYPE: DNA ORGANISM: Artificial Application US/10527552 primer of cephalosporin

US-10-048-046-2 (1-664) x US-10-527-552-18 (1-20) 6.00 100.00% 100.00% Mismatches Indels: Gaps: Conservative: Matches: 000008

APPLICANT: LYNCH, THOMAS J.
APPLICANT: MEYERSON, MATTHEW
APPLICANT: MEXERSON, MATTHEW
APPLICANT: SELLERS, WILLIAM R.
APPLICANT: SETILEMAN, JEFFREY B.
APPLICANT: SETILEMAN, JEFFREY B.
APPLICANT: SOUDELLA, RAFFABLLA
APPLICANT: SOUDELLA, RAFFABLLA
APPLICANT: SOUDELLA, RAFFABLLA
APPLICANT: SOUDELLA, RAFFABLLA
APPLICANTION: ENTHOD TO DETERMINE RESPONSIVENESS OF CANCER TO
TITLE OF INVENTION: TREATMENTS
TITLE OF INVENTION: TREATMENTS
TITLE OF INVENTION: TREATMENTS
FILE REFERENCE: 03025-055147
CURRENT APPLICATION NUMBER: US/11/294,621
CURRENT APPLICATION NUMBER: FCT/US05/010645
PRIOR APPLICATION NUMBER: 60/558,218
PRIOR APPLICATION NUMBER: 60/558,218
PRIOR APPLICATION NUMBER: 60/558,218
PRIOR APPLICATION NUMBER: 60/558,218
PRIOR APPLICATION NUMBER: 60/561,95
PRIOR PILING DATE: 2004-03-31
PRIOR PILING DATE: 2004-04-09
PRIOR PILING DATE: 2004-04-07 Sequence 70, Application US/11294621 GENERAL INFORMATION: APPLICANT: HABER, DANIEL A.
APPLICANT: JANNE, PASI ANTERO
APPLICANT: JOHNSON, BRUCE B. PILING DATE: 2004-04-27
APPLICATION NUMBER: 60/565,985
PILING DATE: 2004-04-27 APPLICATION NUMBER: 60/574,035 DAPHNE WINIFRED

```
Percent Similarity:
Best Local Similarity:
Query Match:
RESULT 6
US-60-742-219-4800
IS-60-742-219-4800
IS-60-742-219-4800, Application US/60742219
INFORMATION:
                                                                                                                ક
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          융
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     र्
                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: nucleic'acid for analysis of methylation status of SEQ ID NO:
US-11-317-798-5513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
U8-11-317-798-5513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-048-046-2 (1-664) x US-11-294-621-70 (1-20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / ORGANISM: Homo sapiens
US-11-294-621-70
                                                                                                                                                    US-10-048-046-2 (1-664) x US-11-317-798-5513 (1-20)
                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2004-06-07
PRIOR APPLICATION NUMBER: 60/592,287
PRIOR FILING DATE: 2004-07-29
NUMBER OF SEQ ID NOS: 762
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5513
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US04/20336
PRIOR FILING DATE: 2004-06-23
PRIOR APPLICATION NUMBER: US 10/602,494
PRIOR FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: EP 04090175.3
PRIOR FILING DATE: 2004-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lofton-Day, Cathy, Model, Fabian; Sledziewski, APPLICANT: Andrew, Rujan, Tamas; Lewin, Joern; Distler, Juerge TITLE OF INVENTION: Methods and nucleic acids for the analysis TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: EP 04090072.2
PRIOR PILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 14624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/317,798
CURRENT FILING DATE: 2005-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 10/603,138 PRIOR FILING DATE: 2003-06-23
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE: bisulfite treated:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 20
                                                                                                         394 ValArgArgSerPheSer 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 ThreerThreerGlyThr 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTTCCACCTCGGGCACA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/11317798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926
6.00
100.00%
100.00%
0.90%
                                                                                                                                                                                              926
6.00
100.00%
100.00%
0.90%
                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
                                                                                                                                                                                            000008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Juergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of colon cell
                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                    Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
RESULT 8
US-11-130-645B-10537
US-11-130-645B-10537, Application US/11130645B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                         ; TYPE: RNA; Homo sapiens US-11-130-645B-8449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-130-645B-8449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-048-046-2 (1-664) x US-60-742-219-4800 (1-21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                       US-10-048-046-2 (1-664) x US-11-130-645B-8449 (1-22)
                                                                                                                                                                                                                                              Pred. No.: .
                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-60-742-219-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                    SOPTWARE: PatentIn version 3.3
SEQ ID NO 8449
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8449, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THER
FILE REFERENCE: 06087,0202,CPUS.13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: Patentin version 3.3
SEQ ID NO 4800
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Berdewegh Paul Van
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis
FILE REFERENCE: 306522-2000
CURRENT APPLICATION NUMBER: US/60/742,219
CURRENT FILLING DATE: 2005-12-05
CURRENT FILLING DATE: 2005-12-05
CURRENT FILLING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 760616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 SerSerLeuGluProGln 248
                                                                            4
                                                                                                       3 ArgProGluGluGlyLys 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 recreectydadecacad 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Belouchi, Abdelmajid
Raelson, John Verner
Bradley, Walter Edward
Paquin, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nguyen-Huu, Quynh
Croteau, Pascal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cousineau,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEETO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Randall David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rene
                                                                                                                                                                                6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
0.90%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           967
                                                                                                                                                                                                                                            1.01e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johanne
                                                                                                                                                                                                                                                                                                                                                                                                                                              AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                 Mismatches:
Indels:
                                                                                                                                                                                                              Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                     000062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000002
```

```
Sequence 13922, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
ITITLE OF INVENTION: MICHORNAS AND USES THEREOF
FILE REFERENCE: 06087,0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF 8EQ ID NOS: 760616 -
SOFTWARE: Patentin version 3.3
SEQ ID NO 13922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-130-645B-10712/c

| Sequence 10712, Application US/11130645B
| GENERAL INFORMATION:
| APPLICANT: ROSETTA GENOMICS LTD
| TITLE OF INVENTION: MICRORNAS AND USES THEREOF
| FILE REFERENCE: 06087.0202.CFUS13
| CURRENT APPLICATION NUMBER: US/11/130,645B
| CURRENT FILING DATE: 2005-05-16
                                                                                                                                                                                                                                                                                                                                       ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Homo sapiens
US-11-130-645B-10537
                                                                                                                                                                                                                                              RESULT 10
U8-11-130-645B-13922
                                                                                                                                                                                                                                                                                                                                                                           US-10-048-046-2 (1-664) x US-11-130-645B-10712 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: RNA; Homo sapiens US-11-130-645B-10712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-048-046-2 (1-664) x US-11-130-645B-10537 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 760616
SOPTWARE: PatentIn version 3.3
SEQ ID NO 10712
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
RUMBER OF SEQ ID NOS: 750616
SOFTWARE: Patentin version 3.3
SEQ ID NO 10537
LENGTH: 23
LENGTH: 22
TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 ProSerProAlaGlyArg 200
                                                                                                                                                                                                                                                                                                                                         452 GlyAlaProGlnAlaLeu 457
                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cccucuccuacuaeacax 22
                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
0.90%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.01e+03
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.01e+03
6.00
100.00#
100.00#
0.90#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                  000002
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                          RESULT 12 ...
US-11-130-645B-13926
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-046-2 (1-664) x US-11-130-645B-13924 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-130-645B-13924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-11-130-645B-13924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-048-046-2 (1-664) x US-11-130-645B-13922 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-130-645B-13922
                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                   US-11-130-645B-13926
                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13924, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CFUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT JILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
                                                                                                                                                                                                   Sequence 13926, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
RUMBER OF SEC. ID NOS: 760616
                                                                                                                                                            SOPTWARE: PatentIn version 3.3
SEQ ID NO 13926
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.3 SEQ ID NO 13924
                                                                                                                             TYPE: RNA
ORGANISM: Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BNGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 AsplysSerArgSerGlu 373
                                                                                                                                                                                                                                                                                                                                                                                               368 AsplysSerArgSerGlu 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GAUAAGUCAAGGUCUGAA
                                                                                                                                                                                                                                                                                                                                                                      5 GAUNAGUCANGGUCUGAN 22
       100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.01e+03
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.01e+03
6.00
100.00%
100.00%
0.90%
                                                                       1.01e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
                                             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0000 N
      000002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .o.o o o o N
```

14

US-10-048-046-2 (1-664) x US-11-130-645B-13926 (1-22)

368

AspLysSerArgSerGlu 373

ū

```
US-10-515-051-78

Sequence 78, Application US/10515051

Sequence 78, Application US/10515051

APPLICANT: OHNO, Ryozo

APPLICANT: TSURUO, Takashi

APPLICANT: NAKAMURA, YUSUKe

TITLE OF INVENTION: METHOD FOR JUDGING SENSIBILITY TO IMATINIB

FILE REFERENCE: 0760-0342PUS1

CURRENT APPLICATION NUMBER: US/10/515,051

CURRENT APPLICATION NUMBER: US/10/515,051

CURRENT APPLICATION NUMBER: DET/JP03/06330

PRIOR APPLICATION NUMBER: PCT/JP03/06330

PRIOR FILING DATE: 2003-05-21

NUMBER OF SEQ ID NOS: 154

SEQ ID NO 78

LENGTH: 23

TUREN: DNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16045, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
ITILE OF INVENTION: MICRORUAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: Patentin version 3.3
SEQ ID NO 16045
LENGTH: 22
TYPE: RNA
ORGANISM: Homo sapiens
US-11-130-645B-16045
                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
밁
                             ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                          OTHER INFORMATION: Oligonucleotide reverse primer used for amplifying human CTSG cD;
OTHER INFORMATION: A
US-10-515-051-78
                                                               US-10-048-046-2 (1-664) x US-10-515-051-78 (1-23)
                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-048-046-2 (1-664) x US-11-130-645B-16045 (1-22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U8-11-130-645B-16045
                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence PRATURE:
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 ValProProSerSerPro 166
                             17 GlyArgLeuLeuArgLeu 22
GGACGITTATTAAGGCTC 21
                                                                                                                    100.00%
                                                                                                                                                                       1.05e+03
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.01e+03
6.00
100.00%
100.00%
0.90%
                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                   ၀၀၀၀၈ည္
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000000
```

Search completed: January 12, 2006, 13:31:58 Job time : 130 secs